

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/684,883A
Source: FW16
Date Processed by STIC: 4/16/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 04/16/2007

PATENT APPLICATION: US/09/684,883A

TIME: 19:14:58

Input Set : E:\417c1.app.txt

Output Set: N:\CRF4\04162007\I684883A.raw

4 <110> APPLICANT: Brodeur, Bernard R.
 5 Martin, Denis
 6 Martin, Josee
 7 Rioux, Clement
 9 <120> TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
 10 OF NEISSERIA MENINGITIDIS
 13 <130> FILE REFERENCE: 484112.417C1
 15 <140> CURRENT APPLICATION NUMBER: US 09/684,883A
 16 <141> CURRENT FILING DATE: 2000-10-06
 18 <150> PRIOR APPLICATION NUMBER: US 08/913,362
 19 <151> PRIOR FILING DATE: 1997-11-13
 21 <150> PRIOR APPLICATION NUMBER: PCT/CA96/00157
 22 <151> PRIOR FILING DATE: 1996-03-15
 24 <150> PRIOR APPLICATION NUMBER: US 60/001,983
 25 <151> PRIOR FILING DATE: 1995-08-04
 27 <150> PRIOR APPLICATION NUMBER: US 08/406,362
 28 <151> PRIOR FILING DATE: 1995-03-17
 30 <160> NUMBER OF SEQ ID NOS: 34
 32 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 830
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Neisseria meningitidis
 39 <220> FEATURE:
 40 <221> NAME/KEY: CDS
 41 <222> LOCATION: (143)...(667)
 43 <220> FEATURE:
 44 <221> NAME/KEY: sig_peptide
 45 <222> LOCATION: (143)...(199)
 47 <220> FEATURE:
 48 <221> NAME/KEY: mat_peptide
 49 <222> LOCATION: (200)...(667)
 51 <400> SEQUENCE: 1
 52 tcggcaaaagc agccggatcac cgctacgtat cttgaagtat tgaaaatatt acgatgcaaa 60
 53 aaagaaaatt taagtataat acagcaggat tctttaacgg attcttaaca atttttctaa 120
 54 ctgaccataa aggaacccaaa at atg aaa aaa gca ctt gcc aca ctg att gcc 172
 55 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala
 56 -15 -10
 58 ctc gct ctc ccg gcc gcc gca ctg gcg gaa ggc gca tcc ggc ttt tac 220
 59 Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr
 60 -5 1 5
 62 gtc caa gcc gat gcc gca cac gca aaa gcc tca agc tct tta ggt tct 268
 63 Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu Gly Ser

see p. 6

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64          10          15          20
66 gcc aaa ggc ttc agc ccg cgc atc tcc gca ggc tac cgc atc aac gac 316
67 Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp
68          25          30          35
70 ctc cgc ttc gcc gtc gat tac acg cgc tac aaa aac tat aaa gcc cca 364
71 Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro
72 40          45          50          55
74 tcc acc gat ttc aaa ctt tac agc atc ggc gcg tcc gcc att tac gac 412
75 Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp
76          60          65          70
78 ttc gac acc caa tcg ccc gtc aaa ccg tat ctc ggc gcg cgc ttg agc 460
79 Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser
80          75          80          85
82 ctc aac cgc gcc tcc gtc gac ttg ggc ggc agc gac agc ttc agc caa 508
83 Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln
84          90          95          100
86 acc tcc atc ggc ctc ggc gta ttg acg ggc gta agc tat gcc gtt acc 556
87 Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr Ala Val Thr
88 105          110          115
90 ccg aat gtc gat ttg gat gcc ggc tac cgc tac aac tac atc ggc aaa 604
91 Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys
92 120          125          130          135
94 gtc aac act gtc aaa aac gtc cgt tcc ggc gaa ctg tcc gtc ggc gtg 652
95 Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Val Gly Val
96          140          145          150
98 cgc gtc aaa ttc tga tatgcgcctt attctgcaaa ccgccgagcc ttcggcggtt 707
99 Arg Val Lys Phe *
100          155
102 ttgttttctg ccaccgcaac tacacaagcc ggcggttttg tacgataatc ccgaatgctg 767
103 cggcttctgc cgccctatctt tttaggaat ccgaaatgac caaaaccatc atccacaccg 827
104 aca 830
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 174
108 <212> TYPE: PRT
109 <213> ORGANISM: Neisseria meningitidis
111 <220> FEATURE:
112 <221> NAME/KEY: SIGNAL
113 <222> LOCATION: (1)...(19)
115 <400> SEQUENCE: 2
116 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala
117          -15          -10          -5
118 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
119          1          5          10
120 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
121 15          20          25
122 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
123 30          35          40          45
124 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu
125          50          55          60

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126 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
127          65          70          75
128 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
129          80          85          90
130 Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile Gly Leu Gly
131          95          100          105
132 Val Leu Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
133 110          115          120          125
134 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
135          130          135          140
136 Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe
137          145          150          155
140 <210> SEQ ID NO: 3
141 <211> LENGTH: 710
142 <212> TYPE: DNA
143 <213> ORGANISM: Neisseria meningitidis
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (116)...(643)
149 <220> FEATURE:
150 <221> NAME/KEY: sig_peptide
151 <222> LOCATION: (116)...(172)
153 <220> FEATURE:
154 <221> NAME/KEY: mat_peptide
155 <222> LOCATION: (173)...(643)
157 <400> SEQUENCE: 3
158 gtatcttgag gcattgaaaa tattacaatg caaaaagaaa atttcagtat aatacggcag 60
159 gattctttaa cggattctta accatttttc tccctgacca taaaggaatc aagat atg 118
160                                     Met
163 aaa aaa gca ctt gcc gca ctg att gcc ctc gcc ctc ccg gcc gcc gca 166
164 Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala Ala
165          -15          -10          -5
167 ctg gcg gaa ggc gca tcc ggc ttt tac gtc caa gcc gat gcc gca cac 214
168 Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His
169          1          5          10
171 gcc aaa gcc tca agc tct tta ggt tct gcc aaa ggc ttc agc ccg cgc 262
172 Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro Arg
173 15          20          25          30
175 atc tcc gca ggc tac cgc atc aac gac ctc cgc ttc gcc gtc gat tac 310
176 Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr
177          35          40          45
179 acg cgc tac aaa aac tat aaa caa gtc cca tcc acc gat ttc aaa ctt 358
180 Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys Leu
181          50          55          60
183 tac agc atc ggc gcg tcc gcc att tac gac ttc gac acc caa tcc ccc 406
184 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
185          65          70          75
187 gtc aaa ccg tat ctc ggc gcg cgc ttg agc ctc aac cgc gcc tcc gtc 454
188 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val

```

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189      80      85      90
191 gac ttt aac ggc agc gac agc ttc agc caa acc tcc acc ggc ctc ggc 502
192 Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly
193 95      100      105      110
195 gta ttg gcg ggc gta agc tat gcc gtt acc ccg aat gtc gat ttg gat 550
196 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
197      115      120      125
199 gcc ggc tac cgc tac aac tac atc ggc aaa gtc aac act gtc aaa aat 598
200 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
201      130      135      140
203 gtc cgt tcc ggc gaa ctg tcc gcc ggc gta cgc gtc aaa ttc tga 643
204 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe *
205      145      150      155
207 tatacgcgtt attccgcaaa ccgcccagcc ttccggcggt tttgttttcc gccgccgcaa 703
208 ctacaca 710
210 <210> SEQ ID NO: 4
211 <211> LENGTH: 175
212 <212> TYPE: PRT
213 <213> ORGANISM: Neisseria meningitidis
215 <220> FEATURE:
216 <221> NAME/KEY: SIGNAL
217 <222> LOCATION: (1)...(19)
219 <400> SEQUENCE: 4
220 Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala
221      -15      -10      -5
222 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
223      1      5      10
224 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
225      15      20      25
226 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
227 30      35      40      45
228 Tyr Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys
229      50      55      60
230 Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser
231      65      70      75
232 Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser
233      80      85      90
234 Val Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu
235      95      100      105
236 Gly Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu
237 110      115      120      125
238 Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys
239      130      135      140
240 Asn Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
241      145      150      155
244 <210> SEQ ID NO: 5
245 <211> LENGTH: 850
246 <212> TYPE: DNA
247 <213> ORGANISM: Neisseria meningitidis

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249 <220> FEATURE:
250 <221> NAME/KEY: CDS
251 <222> LOCATION: (208)...(732)
253 <220> FEATURE:
254 <221> NAME/KEY: sig_peptide
255 <222> LOCATION: (208)...(264)
257 <220> FEATURE:
258 <221> NAME/KEY: mat_peptide
259 <222> LOCATION: (265)...(732)
261 <400> SEQUENCE: 5
262 caccatccg ccgctgatg ccgccaccac catttaaagg caacgcgcgg gttaacggct 60
263 ttgccgtcgg caaagcagcc ggataccgct acgtatcttg aagtattaaa aatattacga 120
264 tgcaaaaaga aaatttaagt ataataaagc agaattcttt aacggattct taacaatttt 180
265 tctaactgac cataaaggaa ccaaaat atg aaa aaa gca ctt gcc aca ctg att 234
266                                     Met Lys Lys Ala Leu Ala Thr Leu Ile
267                                     -15
269 gcc ctc gct ctc ccg gcc gcc gca ctg gcg gaa ggc gca tcc ggc ttt 282
270 Ala Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly Phe
271 -10                               -5                               1                               5
273 tac gtc caa gcc gat gcc gca cac gca aaa gcc tca agc tct tta ggt 330
274 Tyr Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu Gly
275                               10                               15                               20
277 tct gcc aaa ggc ttc agc ccg cgc atc tcc gca ggc tac cgc atc aac 378
278 Ser Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn
279                               25                               30                               35
281 gac ctc cgc ttc gcc gtc gat tac acg cgc tac aaa aac tat aaa gcc 426
282 Asp Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala
283                               40                               45                               50
285 cca tcc acc gat ttc aaa ctt tac agc atc ggc gcg tcc gcc att tac 474
286 Pro Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr
287 55                               60                               65                               70
289 gac ttc gac acc caa tcg ccc gtc aaa ccg tat ctc ggc gcg cgc ttg 522
290 Asp Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu
291                               75                               80                               85
293 agc ctc aac cgc gcc tcc gtc gac ttg ggc ggc agc gac agc ttc agc 570
294 Ser Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser
295                               90                               95                               100
297 caa acc tcc acc ggc ctc ggc gta ttg gcg ggc gta agc tat gcc gtt 618
298 Gln Thr Ser Thr Gly Leu Gly Val Leu Ala Gly Val Ser Tyr Ala Val
299                               105                               110                               115
301 acc ccg aat gtc gat ttg gat gcc ggc tac cgc tac aac tac atc ggc 666
302 Thr Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly
303                               120                               125                               130
305 aaa gtc aac act gtc aaa aac gtc cgt tcc ggc gaa ctg tcc gcc ggt 714
306 Lys Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Ala Gly
307 135                               140                               145                               150
309 gtg cgc gtc aaa ttc tga tatgcgcctt attctgcaaa ccgccgagcc 762
310 Val Arg Val Lys Phe *
311                               155

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/684,883A

DATE: 04/16/2007
TIME: 19:14:59

FJI

Input Set : E:\417c1.app.txt
Output Set: N:\CRF4\04162007\I684883A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:30; Xaa Pos. 7,73,126

VERIFICATION SUMMARY

DATE: 04/16/2007

PATENT APPLICATION: US/09/684,883A

TIME: 19:14:59

Input Set : E:\417c1.app.txt

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L:689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0

M:341 Repeated in SeqNo=30